



sequence listing 09-237,981.ST25
SEQUENCE LISTING

<110> Quertermous, Thomas
Hogan, Brigid
Snodgrass, Ralph H
Zupancic, Thomas J

<120> Antibodies Binding to Polypeptides Encoded by
Developmentally-Regulated Endothelial Cell Locus-1

<130> 213-0094US

<140> US 09/237,981

<141> 1999-01-25

<150> US 08/659,235

<151> 1996-06-05

<150> US 08/480,229

<151> 1995-06-07

<160> 33

<170> PatentIn version 3.2

<210> 1

<211> 81

<212> PRT

<213> Mus sp.

<400> 1

Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala
1 5 10 15

Lys Asp Phe Gly Asp Val Leu Phe Val Gly Ser Tyr Lys Leu Ala Tyr
20 25 30

Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys Gln Arg
35 40 45

Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys
50 55 60

Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu Pro
65 70 75 80

Leu

<210> 2

<211> 81

<212> PRT

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<213> Homo sapiens

<400> 2

Asp Leu Gly Ser Ser Lys Glu Val Thr Gly Ile Ile Thr Gln Gly Ala
1 5 10 15

Arg Asn Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys Val Ala Tyr
20 25 30

Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg Thr Gly
35 40 45

Ser Ser Lys Val Phe Gln Gly Asn Leu Asp Asn Asn Ser His Lys Lys
50 55 60

Asn Ile Phe Glu Lys Pro Phe Met Ala Arg Tyr Val Arg Val Leu Pro
65 70 75 80

Val

<210> 3

<211> 81

<212> PRT

<213> homo sapiens

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Asp Leu Leu Lys Ile Lys Lys Ile Thr Ala Ile Ile Thr Gln Gly Cys
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Lys Ser Leu Ser Ser Glu Met Tyr Val Lys Ser Tyr Thr Ile His Tyr
20 25 30

Ser Glu Gln Gly Val Glu Trp Lys Pro Tyr Arg Leu Lys Ser Ser Met
35 40 45

Val Asp Lys Ile Phe Glu Gly Asn Thr Asn Thr Lys Gly His Val Lys
50 55 60

Asn Phe Phe Asn Pro Pro Ile Ile Ser Arg Phe Ile Arg Val Ile Pro
65 70 75 80

Lys

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<210> 4
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<400> 4

Asp Leu Gln Lys Thr Met Lys Val Thr Gly Ile Ile Thr Gln Gly Val
 1 5 10 15

Lys Ser Leu Phe Thr Ser Met Phe Val Lys Glu Phe Leu Ile Ser Ser
 20 25 30

Ser Gln Asp Gly His His Trp Thr Gln Ile Leu Tyr Asn Gly Lys Val
 35 40 45

Lys Val Phe Gln Gly Asn Gln Asp Ser Ser Thr Pro Met Met Asn Ser
 50 55 60

Leu Asp Pro Pro Leu Leu Thr Arg
 65 70

<210> 5
 <211> 83
 <212> PRT
 <213> Xenopus sp.

<400> 5

Asp Leu Glu Asn Leu Arg Phe Val Ser Gly Ile Gly Thr Gln Gly Ala
 1 5 10 15

Ile Ser Lys Glu Thr Lys Lys Lys Tyr Phe Val Lys Ser Tyr Lys Val
 20 25 30

Asp Ile Ser Ser Asn Gly Glu Asp Trp Ile Thr Leu Lys Asp Gly Asn
 35 40 45

Lys His Leu Val Phe Thr Gly Asn Thr Asp Ala Thr Asp Val Val Tyr
 50 55 60

Arg Pro Phe Ser Lys Pro Val Ile Thr Arg Phe Val Arg Leu Arg Pro
 65 70 75 80

Val Thr Trp

<210> 6

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<211> 79
 <212> PRT
 <213> xenopus sp.

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Asp Leu Ala Glu Glu Lys Ile Val Arg Gly Val Ile Ile Gln Gly Gly
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Lys His Lys Glu Asn Lys Val Phe Met Arg Lys Phe Lys Ile Gly Tyr
 20 25 30

Ser Asn Asn Gly Thr Glu Trp Glu Met Ile Met Asp Ser Ser Lys Asn
 35 40 45

Lys Pro Lys Thr Phe Glu Gly Asn Thr Asn Tyr Asp Thr Pro Glu Leu
 50 55 60

Arg Thr Phe Ala His Ile Thr Thr Gly Phe Ile Arg Ile Ile Pro
 65 70 75

<210> 7
 <211> 75
 <212> PRT
 <213> homo sapiens

<400> 7

Gly Cys Glu Val Pro Arg Thr Phe Met Cys Val Ala Leu Gln Gly Arg
 1 5 10 15

Gly Asp Ala Asp Gln Trp Val Thr Ser Tyr Lys Ile Arg Tyr Ser Leu
 20 25 30

Asp Asn Val Ser Trp Phe Glu Tyr Arg Asn Gly Ala Ala Ile Thr Gly
 35 40 45

Val Thr Asp Arg Asn Thr Val Val Asn His Phe Phe Asp Thr Pro Ile
 50 55 60

Arg Ala Arg Ser Ile Ala Ile His Pro Leu Thr
 65 70 75

<210> 8
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Xaa Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Phe Val Xaa Ser Tyr Lys Ile
 20 25 30

Xaa Tyr Ser Xaa Asp Gly Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45

Xaa Xaa Lys Xaa Lys Val Phe Xaa Gly Asn Thr Asp Xaa Xaa Thr Xaa
 50 55 60

Xaa Xaa Asn Xaa Phe Xaa Xaa Pro Ile Xaa Xaa Arg Phe Ile Arg Xaa
 65 70 75 80

Xaa Pro Xaa Xaa Xaa
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<210> 9
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<221> CDS

<222> (619)..(2058)

<400> 9

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cctgcgtctc atatttctgc atgctgcttt gtttgtatat agtgcgctcc tggcctcagg 180

ctcgcctccc tccagctctc gcttcattgt tctccaagtc agaagcccc gcacccgccc 240

cgcagcagcg tgagccgtag tcaactgctgg ccgcttcgcc tgcgtgcgcg cacggaaatc 300

ggggagccag gaaccaagg agccgccgctc cgcccgtgt gcctctgcta gaccactcgc 360

agccccagcc tctctcaagc gcacccacct ccgcgcaccc cagctcaggc gaagctggag 420

tgaggggtgaa tcaccctttc tctagggcca ccactctttt atcgcccttc ccaagatttg 480

agaagcgctg cgggaggaaa gacgtcctct tgatctctga cagggcgggg ttactgctg 540

tcctgcaggc gcgcctcgcc tactgtgccc tccgctacga ccccggaacca gccaggtca 600

cgctccgtgag aagggatc atg aag cac ttg gta gca gcc tgg ctt ttg gtt 651

Met Lys His Leu Val Ala Ala Trp Leu Leu Val
1 5 10

gga ctc agc ctc ggg gtg ccc cag ttc ggc aaa ggt gac att tgc aac 699

Gly Leu Ser Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn
15 20 25

ccg aac ccc tgt gaa aat ggt ggc atc tgt ctg tca gga ctg gct gat 747

Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp
30 35 40

gat tcc ttt tcc tgt gag tgt cca gaa ggc ttc gca ggt ccg aac tgc 795

Asp Ser Phe Ser Cys Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys
45 50 55

tct agt gtt gtg gag gtt gca tca gat gaa gaa aag cct act tca gca 843

Ser Ser Val Val Glu Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala
60 65 70 75

ggt ccc tgc atc cct aac cca tgc cat aac gga gga acc tgt gag ata 891

Gly Pro Cys Ile Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile
80 85 90

agc gaa gcc tat cga gga gac aca ttc ata ggc tat gtt tgt aaa tgt 939

Ser Glu Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys
95 100 105

cct cgg gga ttt aat ggg att cac tgt cag cac aat ata aat gaa tgt 987

Pro Arg Gly Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys
110 115 120

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gaa gct gag cct tgc aga aat ggc gga ata tgt acc gac ctt gtt gct Glu Ala Glu Pro Cys Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala 125 130 135	1035
aac tac tct tgt gaa tgc cca gga gaa ttt atg gga cga aat tgt caa Asn Tyr Ser Cys Glu Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln 140 145 150 155	1083
tat aaa tgc tct ggg cac ttg gga atc gaa ggt ggg atc ata tct aat Tyr Lys Cys Ser Gly His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn 160 165 170	1131
cag caa atc aca gct tca tct aat cac cga gct ctt ttt gga ctc cag Gln Gln Ile Thr Ala Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln 175 180 185	1179
aag tgg tat ccc tac tat gct cga ctt aat aag aag ggc ctt ata aat Lys Trp Tyr Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn 190 195 200	1227
gcc tgg aca gct gct gaa aat gac aga tgg cca tgg att cag ata aat Ala Trp Thr Ala Ala Glu Asn Asp Arg Trp Pro Trp Ile Gln Ile Asn 205 210 215	1275
ttg caa aga aaa atg aga gtc act ggt gtt att acc caa gga gca aaa Leu Gln Arg Lys Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys 220 225 230 235	1323
agg att gga agc cca gag tac ata aaa tcc tac aaa att gcc tac agc Arg Ile Gly Ser Pro Glu Tyr Ile Lys Ser Tyr Lys Ile Ala Tyr Ser 240 245 250	1371
aat gac ggg aag acc tgg gca atg tac aaa gta aaa ggc acc aat gaa Asn Asp Gly Lys Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu 255 260 265	1419
gag atg gtc ttt cgt gga aat gtt gat aac aac aca cca tat gct aat Glu Met Val Phe Arg Gly Asn Val Asp Asn Asn Thr Pro Tyr Ala Asn 270 275 280	1467
tct ttc aca ccc cca atc aaa gct cag tat gta aga ctc tac ccc caa Ser Phe Thr Pro Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln 285 290 295	1515
att tgt cga agg cat tgt act tta aga atg gaa ctt ctt ggc tgt gag Ile Cys Arg Arg His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu 300 305 310 315	1563
ctc tca ggc tgt tca gaa cct ttg ggg atg aaa tca ggg cat ata caa Leu Ser Gly Cys Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln 320 325 330	1611
gac tac cag atc act gcc tcc agc gtc ttc aga aca ctc aac atg gac Asp Tyr Gln Ile Thr Ala Ser Ser Val Phe Arg Thr Leu Asn Met Asp 335 340 345	1659
atg ttt act tgg gaa cca agg aaa gcc agg ctg gac aag caa ggc aaa Met Phe Thr Trp Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys 350 355 360	1707

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gta aat gcc tgg act tcc ggc cat aac gac cag tca caa tgg tta cag 1755
Val Asn Ala Trp Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln
365 370 375

gtt gat ctt ctt gtc cct act aag gtg aca ggc atc att aca caa gga 1803
Val Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly
380 385 390 395

gct aaa gat ttt ggt cac gtg cag ttt gtt ggg tca tac aaa cta gct 1851
Ala Lys Asp Phe Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala
400 405 410

tac agc aat gat gga gaa cac tgg atg gtg cac cag gat gaa aaa cag 1899
Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys Gln
415 420 425

agg aaa gac aag gtt ttt caa ggc aat ttt gac aat gac act cac agg 1947
Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg
430 435 440

aaa aat gtc atc gac cct ccc atc tat gca cga ttc ata aga atc ctt 1995
Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu
445 450 455

cct tgg tcc tgg tat gga agg atc act ctg cgg tca gag ctg ctg ggc 2043
Pro Trp Ser Trp Tyr Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly
460 465 470 475

tgc gca gag gag gaa tgaagtgcgg ggccgcacat cccacaatgc ttttctttat 2098
Cys Ala Glu Glu Glu
480

tttcctataa gtatctccac gaaatgaact gtgtgaagct gatggaaact gcatttgttt 2158

ttttcaaagt gttcaaatta tggtaggcta ctgactgtct ttttaggagt tctaagcttg 2218

cctttttaat aatttaattt ggtttccttt gctcaactct cttatgtaat atcacactgt 2278

ctgtgagtta ctcttcttgt tctct 2303

<210> 10

<211> 480

<212> PRT

<213> Mus sp.

<400> 10

Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser Leu Gly
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Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro Cys Glu
20 25 30

Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe Ser Cys
35 40 45

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Glu	Cys	Pro	Glu	Gly	Phe	Ala	Gly	Pro	Asn	Cys	Ser	Ser	Val	Val	Glu	50	55	60	
Val	Ala	Ser	Asp	Glu	Glu	Lys	Pro	Thr	Ser	Ala	Gly	Pro	Cys	Ile	Pro	65	70	75	80
Asn	Pro	Cys	His	Asn	Gly	Gly	Thr	Cys	Glu	Ile	Ser	Glu	Ala	Tyr	Arg	85	90	95	
Gly	Asp	Thr	Phe	Ile	Gly	Tyr	Val	Cys	Lys	Cys	Pro	Arg	Gly	Phe	Asn	100	105	110	
Gly	Ile	His	Cys	Gln	His	Asn	Ile	Asn	Glu	Cys	Glu	Ala	Glu	Pro	Cys	115	120	125	
Arg	Asn	Gly	Gly	Ile	Cys	Thr	Asp	Leu	Val	Ala	Asn	Tyr	Ser	Cys	Glu	130	135	140	
Cys	Pro	Gly	Glu	Phe	Met	Gly	Arg	Asn	Cys	Gln	Tyr	Lys	Cys	Ser	Gly	145	150	155	160
His	Leu	Gly	Ile	Glu	Gly	Gly	Ile	Ile	Ser	Asn	Gln	Gln	Ile	Thr	Ala	165	170	175	
Ser	Ser	Asn	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln	Lys	Trp	Tyr	Pro	Tyr	180	185	190	
Tyr	Ala	Arg	Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn	Ala	Trp	Thr	Ala	Ala	195	200	205	
Glu	Asn	Asp	Arg	Trp	Pro	Trp	Ile	Gln	Ile	Asn	Leu	Gln	Arg	Lys	Met	210	215	220	
Arg	Val	Thr	Gly	Val	Ile	Thr	Gln	Gly	Ala	Lys	Arg	Ile	Gly	Ser	Pro	225	230	235	240
Glu	Tyr	Ile	Lys	Ser	Tyr	Lys	Ile	Ala	Tyr	Ser	Asn	Asp	Gly	Lys	Thr	245	250	255	
Trp	Ala	Met	Tyr	Lys	Val	Lys	Gly	Thr	Asn	Glu	Glu	Met	Val	Phe	Arg	260	265	270	
Gly	Asn	Val	Asp	Asn	Asn	Thr	Pro	Tyr	Ala	Asn	Ser	Phe	Thr	Pro	Pro				

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275

280

285

Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Ile Cys Arg Arg His
290 295 300

Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys Ser
305 310 315 320

Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile Thr
325 330 335

Ala Ser Ser Val Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp Glu
340 345 350

Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp Thr
355 360 365

Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu Val
370 375 380

Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe Gly
385 390 395 400

His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp Gly
405 410 415

Glu His Trp Met Val His Gln Asp Glu Lys Gln Arg Lys Asp Lys Val
420 425 430

Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp
435 440 445

Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu Pro Trp Ser Trp Tyr
450 455 460

Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly Cys Ala Glu Glu Glu
465 470 475 480

<210> 11
<211> 1780
<212> DNA
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<220>
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<222> (1)..(1779)

<400> 11

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cgc	tga	gga	aag	aga	acg	tct	tct	tga	att	ctt	tag	tag	ggg	cgg	agt	96
Arg		Gly	Lys	Arg	Thr	Ser	Ser		Ile	Leu			Gly	Arg	Ser	
					20								25			
ctg	ctg	ctg	ccc	tgc	gct	gcc	acc	tcg	gct	aca	ctg	ccc	tcc	gcg	acg	144
Leu	Leu		Pro	Cys	Ala	Ala	Thr	Ser	Ala	Thr	Leu	Pro	Ser	Ala	Thr	
		30					35					40				
acc	cct	gac	cag	ccg	ggg	tca	cgt	ccg	gga	gac	ggg	atc	atg	aag	cgc	192
Thr	Pro	Asp	Gln	Pro	Gly	Ser	Arg	Pro	Gly	Asp	Gly	Ile	Met	Lys	Arg	
	45					50					55					
tcg	gta	gcc	gtc	tgg	ctc	ttg	gtc	ggg	ctc	agc	ctc	ggt	gtc	ccc	cag	240
Ser	Val	Ala	Val	Trp	Leu	Leu	Val	Gly	Leu	Ser	Leu	Gly	Val	Pro	Gln	
60					65					70					75	
ttc	ggc	aaa	ggt	gat	att	tgt	gat	ccc	aat	cca	tgt	gaa	aat	gga	ggt	288
Phe	Gly	Lys	Gly	Asp	Ile	Cys	Asp	Pro	Asn	Pro	Cys	Glu	Asn	Gly	Gly	
				80					85					90		
atc	tgt	ttg	cca	gga	ttg	gct	gta	ggt	tcc	ttt	tcc	tgt	gag	tgt	cca	336
Ile	Cys	Leu		Gly	Leu	Ala	Val	Gly	Ser	Phe	Ser	Cys	Glu	Cys	Pro	
			95					100					105			
gat	ggc	ttc	aca	gac	ccc	aac	tgt	tct	agt	gtt	gtg	gag	ggt	gca	tca	384
Asp	Gly	Phe	Thr	Asp	Pro	Asn	Cys	Ser	Ser	Val	Val	Glu	Val	Ala	Ser	
		110					115					120				
gat	gaa	gaa	gaa	cca	act	tca	gca	ggt	ccc	tgc	act	cct	aat	cca	tgc	432
Asp	Glu	Glu	Glu	Pro	Thr	Ser	Ala	Gly	Pro	Cys	Thr	Pro	Asn	Pro	Cys	
	125					130					135					
cat	aat	gga	gga	acc	tgt	gaa	ata	agt	gaa	gca	tac	cga	ggg	gat	aca	480
His	Asn	Gly	Gly	Thr	Cys	Glu	Ile	Ser	Glu	Ala	Tyr	Arg	Gly	Asp	Thr	
140					145					150					155	
ttc	ata	ggc	tat	gtt	tgt	aaa	tgt	ccc	cga	gga	ttt	aat	ggg	att	cac	528
Phe	Ile	Gly	Tyr	Val	Cys	Lys	Cys	Pro	Arg	Gly	Phe	Asn	Gly	Ile	His	
				160					165					170		
tgt	cag	cac	aac	ata	aat	gaa	tgc	gaa	gtt	gag	cct	tgc	aaa	aat	ggt	576
Cys	Gln	His		Ile	Asn	Glu	Cys	Glu	Val	Glu	Pro	Cys	Lys	Asn	Gly	
			175					180					185			
gga	ata	tgt	aca	gat	ctt	gtt	gct	aac	tat	tcc	tgt	gag	tgc	cca	ggc	624
Gly	Ile	Cys	Thr	Asp	Leu	Val	Ala	Asn	Tyr	Ser	Cys	Glu	Cys	Pro	Gly	
			190				195					200				
gaa	ttt	atg	gga	aga	aat	tgt	caa	tac	aaa	tgc	tca	ggc	cca	ctg	gga	672
Glu	Phe	Met	Gly	Arg	Asn	Cys	Gln	Tyr	Lys	Cys	Ser	Gly	Pro	Leu	Gly	
	205					210					215					

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att gaa ggt gga att ata tca aac cag caa atc aca gct tcc tct act Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala Ser Ser Thr 220 225 230 235	720
cac cga gct ctt ttt gga ctc caa aaa tgg tat ccc tac tat gca cgt His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr Tyr Ala Arg 240 245 250	768
ctt aat aag aag ggg ctt ata aat gcg tgg aca gct gca gaa aat gac Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala Glu Asn Asp 255 260 265	816
aga tgg aac cgg tgg att cag ata aat ttg caa aga aaa atg aga gtt Arg Trp Asn Arg Trp Ile Gln Ile Asn Leu Gln Arg Lys Met Arg Val 270 275 280	864
act ggt gtg att acc caa ggg gcc aag agg att gga agc cca gag tat Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser Pro Glu Tyr 285 290 295	912
ata aaa ttc tac aaa att gcc tac agt aat gat gga aag act tgg gca Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys Thr Trp Ala 300 305 310 315	960
atg tac aaa gtg aaa ggc acc aat gaa gac atg gtg ttt cgt gga aac Met Tyr Lys Val Lys Gly Thr Asn Glu Asp Met Val Phe Arg Gly Asn 320 325 330	1008
att gat aac aac act cca tat gct aac tct ttc aca ccc ccc ata aaa Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro Pro Ile Lys 335 340 345	1056
gct cag tat gta aga ctc tat ccc caa gtt tgt cga aga cat tgc act Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val Cys Arg Arg His Cys Thr 350 355 360	1104
ttg cga atg gaa ctt ctt ggc tgt gaa ctg tcg ggt tgt tct gag cct Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys Ser Glu Pro 365 370 375	1152
ctg ggt atg aaa tca gga cat ata caa gac tat cag atc act gcc tcc Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile Thr Ala Ser 380 385 390 395	1200
agc atc ttc aga acg ctc aac atg gac atg ttc act tgg gaa cca agg Ser Ile Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp Glu Pro Arg 400 405 410	1248
aaa gct cgg ctg gac aag caa ggc aaa gtg aat gcc tgg acc tct ggc Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp Thr Ser Gly 415 420 425	1296
cac aat gac cag tca caa tgg tta cag gtg gat ctt ctt gtt cca acc His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu Val Pro Thr 430 435 440	1344
aaa gtg act ggc atc att aca caa gga gct aaa gat ttt ggt cat gta Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe Gly His Val 445 450 455	1392

sequence listing 09-237,981.ST25

cag ttt gtt ggc tcc tac aaa ctg gct tac agc aat gat gga gaa cac	1440
Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp Gly Glu His	
460 465 470 475	
tgg act gta tac cag gat gaa aag caa aga aaa gat aag gtt ttc cag	1488
Trp Thr Val Tyr Gln Asp Glu Lys Gln Arg Lys Asp Lys Val Phe Gln	
480 485 490	
gga aat ttt gac aat gac act cac aga aaa aat gtc atc gac cct ccc	1536
Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp Pro Pro	
495 500 505	
atc tat gca cga cac ata aga atc ctt cct tgg tcc tgg tac ggg agg	1584
Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp Tyr Gly Arg	
510 515 520	
atc aca ttg gcg tca gag ctg ctg ggc tgc aca gag gag gaa tga ggg	1632
Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu Glu Gly	
525 530 535	
gag gct aca ttt cac aac cgt ctt ccc tat ttg ggt aaa agt atc tcc	1680
Glu Ala Thr Phe His Asn Arg Leu Pro Tyr Leu Gly Lys Ser Ile Ser	
540 545 550	
atg gaa tga act gtg taa aat ctg tag gaa act gaa tgg ttt ttt ttt	1728
Met Glu Thr Val Asn Leu Glu Thr Glu Trp Phe Phe Phe	
555 560 565	
ttt tca tga aaa agt ggt caa att atg gta ggc aac taa cgg tgt ttt	1776
Phe Ser Lys Ser Gly Gln Ile Met Val Gly Asn Arg Cys Phe	
570 575 580	
tac c	1780
Tyr	

<210> 12
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 <212> PRT
 <213> homo sapiens

<400> 12

Ser Pro Leu Ser Pro Ser Pro Arg Ile Cys Leu Thr Lys Arg
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<210> 13
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 <212> PRT
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sequence listing 09-237,981.ST25

<210> 14
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 <212> . PRT
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Gly Arg Ser Leu Leu Leu Pro Cys Ala Ala Thr Ser Ala Thr Leu Pro
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Ser Ala Thr Thr Pro Asp Gln Pro Gly Ser Arg Pro Gly Asp Gly Ile
 20 25 30

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly
 35 40 45

Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu
 50 55 60

Asn Gly Gly Ile Cys Leu Pro Gly Leu Ala Val Gly Ser Phe Ser Cys
 65 70 75 80

Glu Cys Pro Asp Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu
 85 90 95

Val Ala Ser Asp Glu Glu Glu Pro Thr Ser Ala Gly Pro Cys Thr Pro
 100 105 110

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
 115 120 125

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
 130 135 140

Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Val Glu Pro Cys
 145 150 155 160

Lys Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
 165 170 175

Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
 180 185 190

Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
 195 200 205

sequence listing 09-237,981.ST25

Ser	Ser	Thr	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln	Lys	Trp	Tyr	Pro	Tyr		
210						215					220						
Tyr	Ala	Arg	Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn	Ala	Trp	Thr	Ala	Ala		
225					230					235					240		
Glu	Asn	Asp	Arg	Trp	Asn	Arg	Trp	Ile	Gln	Ile	Asn	Leu	Gln	Arg	Lys		
				245					250					255			
Met	Arg	Val	Thr	Gly	Val	Ile	Thr	Gln	Gly	Ala	Lys	Arg	Ile	Gly	Ser		
			260					265					270				
Pro	Glu	Tyr	Ile	Lys	Phe	Tyr	Lys	Ile	Ala	Tyr	Ser	Asn	Asp	Gly	Lys		
		275					280					285					
Thr	Trp	Ala	Met	Tyr	Lys	Val	Lys	Gly	Thr	Asn	Glu	Asp	Met	Val	Phe		
	290					295					300						
Arg	Gly	Asn	Ile	Asp	Asn	Asn	Thr	Pro	Tyr	Ala	Asn	Ser	Phe	Thr	Pro		
305					310					315					320		
Pro	Ile	Lys	Ala	Gln	Tyr	Val	Arg	Leu	Tyr	Pro	Gln	Val	Cys	Arg	Arg		
				325					330					335			
His	Cys	Thr	Leu	Arg	Met	Glu	Leu	Leu	Gly	Cys	Glu	Leu	Ser	Gly	Cys		
			340					345					350				
Ser	Glu	Pro	Leu	Gly	Met	Lys	Ser	Gly	His	Ile	Gln	Asp	Tyr	Gln	Ile		
		355					360					365					
Thr	Ala	Ser	Ser	Ile	Phe	Arg	Thr	Leu	Asn	Met	Asp	Met	Phe	Thr	Trp		
	370					375					380						
Glu	Pro	Arg	Lys	Ala	Arg	Leu	Asp	Lys	Gln	Gly	Lys	Val	Asn	Ala	Trp		
385					390					395					400		
Thr	Ser	Gly	His	Asn	Asp	Gln	Ser	Gln	Trp	Leu	Gln	Val	Asp	Leu	Leu		
				405					410					415			
Val	Pro	Thr	Lys	Val	Thr	Gly	Ile	Ile	Thr	Gln	Gly	Ala	Lys	Asp	Phe		
			420					425					430				
Gly	His	Val	Gln	Phe	Val	Gly	Ser	Tyr	Lys	Leu	Ala	Tyr	Ser	Asn	Asp		
		435					440					445					

sequence listing 09-237,981.ST25

Gly Glu His Trp Thr Val Tyr Gln Asp Glu Lys Gln Arg Lys Asp Lys
450 455 460

Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile
465 470 475 480

Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp
485 490 495

Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu
500 505 510

Glu

<210> 15
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<212> PRT
<213> homo sapiens

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Gly Glu Ala Thr Phe His Asn Arg Leu Pro Tyr Leu Gly Lys Ser Ile
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Ser Met Glu

<210> 16
<211> 9
<212> PRT
<213> homo sapiens

<400> 16

Glu Thr Glu Trp Phe Phe Phe Phe Ser
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<210> 17
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<212> PRT
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<400> 17

Lys Ser Gly Gln Ile Met Val Gly Asn
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sequence listing 09-237,981.ST25

<210> 18
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Arg Cys Phe Tyr
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 agcaatgacg ggaagacctg ggcaatgtac aaagtaaaag gcaccaatga agagatggtc 180
 tttcgtggaa atgttgataa caacacacca tatgctaatt ctttcacacc cccaatcaaa 240
 gctcagtatg taagactcta cccccaaatt tgtcgaaggc attgtacttt aagaatggaa 300
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 <211> 316
 <212> PRT
 <213> homo sapiens

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Cys Ser Thr Gln Leu Gly Met Glu Gly Gly Ala Ile Ala Asp Ser Gln
 1 5 10 15

Ile Ser Ala Ser Tyr Val Tyr Met Gly Phe Met Gly Leu Gln Arg Trp
 20 25 30

Gly Pro Glu Leu Ala Arg Leu Tyr Arg Thr Gly Ile Val Asn Ala Trp
 35 40 45

His Ala Ser Asn Tyr Asp Ser Lys Pro Trp Ile Gln Val Asn Leu Leu
 50 55 60

Arg Lys Met Arg Val Ser Gly Val Met Thr Gln Gly Ala Ser Arg Ala
 65 70 75 80

Gly Arg Ala Glu Tyr Leu Lys Thr Phe Lys Val Ala Tyr Ser Leu Asp
 85 90 95

sequence listing 09-237,981.ST25

Gly	Arg	Lys	Phe	Glu	Phe	Ile	Gln	Asp	Glu	Ser	Gly	Gly	Asp	Lys	Glu	100	105	110
Phe	Leu	Gly	Asn	Leu	Asp	Asn	Asn	Ser	Leu	Lys	Val	Asn	Met	Phe	Asn	115	120	125
Pro	Thr	Leu	Glu	Ala	Gln	Tyr	Ile	Arg	Leu	Tyr	Pro	Val	Ser	Cys	His	130	135	140
Arg	Gly	Cys	Thr	Leu	Arg	Phe	Glu	Leu	Leu	Gly	Cys	Glu	Leu	His	Gly	145	150	155
Cys	Leu	Glu	Pro	Leu	Gly	Leu	Lys	Asn	Asn	Thr	Ile	Pro	Asp	Ser	Gln	165	170	175
Met	Ser	Ala	Ser	Ser	Ser	Tyr	Lys	Thr	Trp	Asn	Leu	Arg	Ala	Phe	Gly	180	185	190
Trp	Tyr	Pro	His	Leu	Gly	Arg	Leu	Asp	Asn	Gln	Gly	Lys	Ile	Asn	Ala	195	200	205
Trp	Thr	Ala	Gln	Ser	Asn	Ser	Ala	Lys	Glu	Trp	Leu	Gln	Val	Asp	Leu	210	215	220
Gly	Thr	Gln	Arg	Gln	Val	Thr	Gly	Ile	Ile	Thr	Gln	Gly	Ala	Arg	Asp	225	230	235
Phe	Gly	His	Ile	Gln	Tyr	Val	Glu	Ser	Tyr	Lys	Val	Ala	His	Ser	Asp	245	250	255
Asp	Gly	Val	Gln	Trp	Thr	Val	Tyr	Glu	Glu	Gln	Gly	Ser	Ser	Lys	Val	260	265	270
Phe	Gln	Gly	Asn	Leu	Asp	Asn	Asn	Ser	His	Lys	Lys	Asn	Ile	Phe	Glu	275	280	285
Lys	Pro	Phe	Met	Ala	Arg	Tyr	Val	Arg	Val	Leu	Pro	Val	Ser	Trp	His	290	295	300
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sequence listing 09-237,981.ST25

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 <222> (277)..(277)
 <223> Xaa can be any naturally occurring amino acid

<400> 21

Cys Ser Gly Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln
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 20 25 30

Tyr Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp
 35 40 45

Thr Ala Ala Glu Asn Asp Arg Trp Asn Arg Trp Ile Gln Ile Asn Leu
 50 55 60

sequence listing 09-237,981.ST25

Gln	Arg	Lys	Met	Arg	Val	Thr	Gly	Val	Ile	Thr	Gln	Gly	Ala	Lys	Arg	65	70	75	80
Ile	Gly	Ser	Pro	Glu	Tyr	Ile	Lys	Phe	Tyr	Lys	Ile	Ala	Tyr	Ser	Asn	85	90	95	
Asp	Gly	Lys	Thr	Trp	Ala	Met	Tyr	Lys	Val	Lys	Gly	Thr	Asn	Glu	Asp	100	105	110	
Met	Val	Phe	Arg	Gly	Asn	Ile	Asp	Asn	Asn	Thr	Pro	Tyr	Ala	Asn	Ser	115	120	125	
Phe	Thr	Pro	Pro	Ile	Lys	Ala	Gln	Tyr	Val	Arg	Leu	Tyr	Pro	Gln	Val	130	135	140	
Cys	Arg	Arg	His	Cys	Thr	Leu	Arg	Met	Glu	Leu	Leu	Gly	Cys	Glu	Leu	145	150	155	160
Ser	Gly	Cys	Ser	Glu	Pro	Leu	Gly	Met	Lys	Ser	Gly	His	Ile	Gln	Asp	165	170	175	
Tyr	Gln	Ile	Thr	Ala	Ser	Ser	Ile	Phe	Arg	Thr	Leu	Asn	Met	Asp	Met	180	185	190	
Phe	Thr	Trp	Glu	Pro	Arg	Lys	Ala	Arg	Leu	Asp	Lys	Gln	Gly	Lys	Val	195	200	205	
Asn	Ala	Trp	Thr	Ser	Gly	His	Asn	Asp	Gln	Ser	Gln	Trp	Leu	Gln	Val	210	215	220	
Xaa	Leu	Leu	Val	Pro	Thr	Lys	Val	Thr	Gly	Ile	Ile	Thr	Gln	Gly	Ala	225	230	235	240
Lys	Asp	Xaa	Gly	His	Val	Gln	Phe	Val	Gly	Ser	Tyr	Lys	Leu	Ala	Tyr	245	250	255	
Ser	Asn	Asp	Gly	Glu	His	Trp	Thr	Val	Xaa	Gln	Asp	Glu	Lys	Gln	Arg	260	265	270	
Lys	Asp	Lys	Val	Xaa	Gln	Gly	Asn	Phe	Asp	Asn	Asp	Thr	His	Arg	Lys	275	280	285	
Asn	Val	Ile	Asp	Pro	Pro	Ile	Tyr	Ala	Arg	His	Ile	Arg	Ile	Leu	Pro	290	295	300	

sequence listing 09-237,981.ST25

Trp Ser Trp Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys
305 310 315 320

Thr

<210> 22
<211> 25
<212> PRT
<213> homo sapiens

<400> 22

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly
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Val Pro Gln Phe Gly Lys Gly Asp Ile
20 25

<210> 23
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<212> PRT
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<400> 23

Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Pro Gly Leu
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Ala Val Gly Ser Phe Ser Cys Glu Cys Pro Asp Gly Phe Thr Asp Pro
20 25 30

Asn Cys Ser Ser Val Val Glu Val Ala Ser Asp Glu Glu Glu Pro Thr
35 40 45

Ser Ala Gly Pro
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<210> 24
<211> 45
<212> PRT
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<400> 24

Cys Thr Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu
1 5 10 15

Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg

sequence listing 09-237,981.ST25

20

25

30

Gly Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu
35 40 45

<210> 25
<211> 35
<212> PRT
<213> homo sapiens

<400> 25

Cys Glu Val Glu Pro Cys Lys Asn Gly Gly Ile Cys Thr Asp Leu Val
1 5 10 15

Ala Asn Tyr Ser Cys Glu Cys Pro Gly Glu Phe Met Gly Arg Asn Cys
20 25 30

Gln Tyr Lys
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sequence listing 09-237,981.ST25

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 <223> Y or F

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 <222> (40)..(40)
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<400> 26

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Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Cys	Xaa	Xaa
			20					25					30		

Gly	Xaa	Xaa	Gly	Xaa	Xaa	Cys	Xaa
			35				40

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 <211> 310
 <212> DNA
 <213> homo sapiens

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 <222> (1)..(1)

sequence listing 09-237,981.ST25

<223> n is a, c, g, t or u

<400> 27

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gtggagggtg gtccctgcac tcctaattcca tgccataatg gaggaacctg tgaaataagt    180
gaagcatacc gaggggatac attcataggc tatgtttgta aatgtccccg aggatttaat    240
gggattcact gtcagcacia cataaatgaa tgcgaagttg agccttgcaa aaatggtgga    300
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<220>

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<222> (1819)..(1821)

<223> n is a, c, g, t or u

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ctccagctct cgcttcattg ttctccaagt cagaagcccc cgcacccgcc gcgcagcagc    180
gtgagccgta gtcactgctg gccgcttcgc ctgcgtgcgc gcacggaaat cggggagcca    240
ggaacccaag gagccgccgt ccgcccgcgt tgccctctgct agaccactcg cagccccagc    300
ctctctcaag cgcacccacc tccgcgcacc ccagctcagg cgaagctgga gtgaggggtga    360
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gcgggaggaa agacgtcctc ttgatctctg acagggcggg gtttactgct gtcctgcagg    480
cgcgccctgc ctactgtgcc ctccgctacg accccggacc agcccagggtc acgtccgtga    540
gaagggatc atg aag cac ttg gta gca gcc tgg ctt ttg gtt gga ctc agc    591
      Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser
      1              5              10

ctc ggg gtg ccc cag ttc ggc aaa ggt gac att tgc aac ccg aac ccc    639
Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro
15              20              25              30

tgt gaa aat ggt ggc atc tgt ctg tca gga ctg gct gat gat tcc ttt    687

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sequence listing 09-237,981.ST25

Cys	Glu	Asn	Gly	Gly	Ile	Cys	Leu	Ser	Gly	Leu	Ala	Asp	Asp	Ser	Phe	
				35					40					45		
tcc	tgt	gag	tgt	cca	gaa	ggc	ttc	gca	ggc	ccg	aac	tgc	tct	agt	gtt	735
Ser	Cys	Glu	Cys	Pro	Glu	Gly	Phe	Ala	Gly	Pro	Asn	Cys	Ser	Ser	Val	
			50				55					60				
gtg	gag	gtt	gca	tca	gat	gaa	gaa	aag	cct	act	tca	gca	ggc	ccc	tgc	783
Val	Glu	Val	Ala	Ser	Asp	Glu	Glu	Lys	Pro	Thr	Ser	Ala	Gly	Pro	Cys	
			65				70					75				
atc	cct	aac	cca	tgc	cat	aac	gga	gga	acc	tgt	gag	ata	agc	gaa	gcc	831
Ile	Pro	Asn	Pro	Cys	His	Asn	Gly	Gly	Thr	Cys	Glu	Ile	Ser	Glu	Ala	
	80					85					90					
tat	cga	gga	gac	aca	ttc	ata	ggc	tat	gtt	tgt	aaa	tgt	cct	cgg	gga	879
Tyr	Arg	Gly	Asp	Thr	Phe	Ile	Gly	Tyr	Val	Cys	Lys	Cys	Pro	Arg	Gly	
95					100				105						110	
ttt	aat	ggg	att	cac	tgt	cag	cac	aat	ata	aat	gaa	tgt	gaa	gct	gag	927
Phe	Asn	Gly	Ile	His	Cys	Gln	His	Asn	Ile	Asn	Glu	Cys	Glu	Ala	Glu	
				115					120					125		
cct	tgc	aga	aat	ggc	gga	ata	tgt	acc	gac	ctt	gtt	gct	aac	tac	tct	975
Pro	Cys	Arg	Asn	Gly	Gly	Ile	Cys	Thr	Asp	Leu	Val	Ala	Asn	Tyr	Ser	
			130					135					140			
tgt	gaa	tgc	cca	gga	gaa	ttt	atg	gga	cga	aat	tgt	caa	tat	aaa	tgc	1023
Cys	Glu	Cys	Pro	Gly	Glu	Phe	Met	Gly	Arg	Asn	Cys	Gln	Tyr	Lys	Cys	
			145				150					155				
tct	ggg	cac	ttg	gga	atc	gaa	ggc	ggg	atc	ata	tct	aat	cag	caa	atc	1071
Ser	Gly	His	Leu	Gly	Ile	Glu	Gly	Gly	Ile	Ile	Ser	Asn	Gln	Gln	Ile	
	160					165					170					
aca	gct	tca	tct	aat	cac	cga	gct	ctt	ttt	gga	ctc	cag	aag	tgg	tat	1119
Thr	Ala	Ser	Ser	Asn	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln	Lys	Trp	Tyr	
175					180				185						190	
ccc	tac	tat	gct	aga	ctt	aat	aag	aag	ggc	ctt	ata	aat	gcc	tgg	aca	1167
Pro	Tyr	Tyr	Ala	Arg	Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn	Ala	Trp	Thr	
				195					200				205			
gct	gct	gaa	aat	gac	aga	tgg	cca	tgg	att	cag	gta	aca	gtg	gga		1212
Ala	Ala	Glu	Asn	Asp	Arg	Trp	Pro	Trp	Ile	Gln	Val	Thr	Val	Gly		
			210					215					220			
tgagacaaat	ccatttccca	aattatcaga	atcattatag	aagtaggtta	gggagaattg											1272
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Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe Ser Cys
 35 40 45

Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val Val Glu
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Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys Ile Pro
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Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
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Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn

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Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu Pro Cys		
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Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu		
130	135	140
Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly		
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His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala		
165	170	175
Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr		
180	185	190
Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala		
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 35 40 45

sequence listing 09-237,981.ST25

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Asn	Pro	Cys	His	Asn	Gly	Gly	Thr	Cys	Glu	Ile	Ser	Glu	Ala	Tyr	Arg
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Cys	Pro	Gly	Glu	Phe	Met	Gly	Arg	Asn	Cys	Gln	Tyr	Lys	Cys	Ser	Gly
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Pro	Leu	Gly	Ile	Glu	Gly	Gly	Ile	Ile	Ser	Asn	Gln	Gln	Ile	Thr	Ala
				165					170					175	
Ser	Ser	Thr	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln	Lys	Trp	Tyr	Pro	Tyr
			180					185					190		
Tyr	Ala	Arg	Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn	Ala	Trp	Thr	Ala	Ala
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Pro	Glu	Tyr	Ile	Lys	Phe	Tyr	Lys	Ile	Ala	Tyr	Ser	Asn	Asp	Gly	Lys
				245					250					255	
Thr	Trp	Ala	Met	Tyr	Lys	Val	Lys	Gly	Thr	Asn	Glu	Asp	Met	Val	Phe
			260					265					270		
Arg	Gly	Asn	Ile	Asp	Asn	Asn	Thr	Pro	Tyr	Ala	Asn	Ser	Phe	Thr	Pro

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275

280

285

Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val Cys Arg Arg
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His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys
305 310 315 320

Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile
325 330 335

Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp
340 345 350

Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp
355 360 365

Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Xaa Leu Leu
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Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Xaa
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Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp
405 410 415

Gly Glu His Trp Thr Val Xaa Gln Asp Glu Lys Gln Arg Lys Asp Lys
420 425 430

Val Xaa Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile
435 440 445

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 Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Gly Pro Cys Thr Pro
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 Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
 50 55 60
 Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
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